

SEQUENCE LISTING



<110> Lukyanov, Sergey
 Lukyanov, Konstantin
 Yanushevich, Yuriy
 Savistky, Alexandr
 Fradkov, Arcady

<120> Non Aggregating Fluorescent Proteins and
 Methods for Using the Same

<130> CLON-067

<150> 10/006,922
 <151> 2001-12-04

<150> 60/270,983
 <151> 2001-02-21

<160> 31

<170> FastSEQ for Windows Version 4.0

<210> 1
 <211> 687
 <212> DNA
 <213> Anemonia majano

<400> 1
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 tgtgtcaatg ggcattactt taccgtcaaa ggtgaaggca acgggaagcc atacgaaggg 120
 acgcagaccc cgactttaa agtcaccatg gccaacggtg ggccccttgc attctcctt 180
 gacatactat ctacagtgtt caagtatgga aatcgatgct ttactgcgtt tcctaccagt 240
 atgcccggact atttcaaaaca agcatttcct gacggaatgt catatgaaag gacttttacc 300
 tatgaagatg gaggagttgc tacagccagt tggaaataaa gccttaaagg caactgctt 360
 gaggcacaat ccacgtttca tggagtgaac tttcctgctg atggacctgt gatggcgaag 420
 atgacaactg gttgggaccc atcttttagg aaaatgactg tctgcgtatgg aatattgaag 480
 ggtgatgtca ccgcgttcct catgctgcaa ggaggtggca attacagatg ccaattccac 540
 acttcttaca agacaaaaaaa accggtgacg atgcccaccaa accatgcgtt ggaacatcgc 600
 attgcgagga ccgaccttga caaagggtggc aacagtgttc agctgacgga gcacgctgtt 660
 gcacatataa cctctgttgtt ccctttc 687

<210> 2
 <211> 229
 <212> PRT
 <213> Anemonia majano

<400> 2
 Met Ala Leu Ser Asn Lys Phe Ile Gly Asp Asp Met Lys Met Thr Tyr
 1 5 10 15
 His Met Asp Gly Cys Val Asn Gly His Tyr Phe Thr Val Lys Gly Glu
 20 25 30
 Gly Asn Gly Lys Pro Tyr Glu Gly Thr Gln Thr Ser Thr Phe Lys Val
 35 40 45
 Thr Met Ala Asn Gly Gly Pro Leu Ala Phe Ser Phe Asp Ile Leu Ser
 50 55 60
 Thr Val Phe Lys Tyr Gly Asn Arg Cys Phe Thr Ala Tyr Pro Thr Ser
 65 70 75 80

Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu
 85 90 95
 Arg Thr Phe Thr Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Glu
 100 105 110
 Ile Ser Leu Lys Gly Asn Cys Phe Glu His Lys Ser Thr Phe His Gly
 115 120 125
 Val Asn Phe Pro Ala Asp Gly Pro Val Met Ala Lys Met Thr Thr Gly
 130 135 140
 Trp Asp Pro Ser Phe Glu Lys Met Thr Val Cys Asp Gly Ile Leu Lys.
 145 150 155 160
 Gly Asp Val Thr Ala Phe Leu Met Leu Gln Gly Gly Gly Asn Tyr Arg
 165 170 175
 Cys Gln Phe His Thr Ser Tyr Lys Thr Lys Lys Pro Val Thr Met Pro
 180 185 190
 Pro Asn His Ala Val Glu His Arg Ile Ala Arg Thr Asp Leu Asp Lys
 195 200 205
 Gly Gly Asn Ser Val Gln Leu Thr Glu His Ala Val Ala His Ile Thr
 210 215 220
 Ser Val Val Pro Phe
 225

<210> 3
 <211> 693
 <212> DNA
 <213> Zoanthus sp.

<400> 3
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 tgcgtcgatg gacataaatt tggatcactg ggagagggca ttggatatcc gttcaaaggg 120
 aaacaggcta ttaatctgtg tgggtcgaa ggtggaccat tgccatttgc cgaagacata 180
 ttgtcagctg cctttatgtt cggaaacagg gtttcaactg aatatcctca agacatagct 240
 gactatttca agaactcgtg tcctgctgg tatacatggg acaggcttt tctctttgag 300
 gatggagcag tttgcatatg taatgcagat ataacagtga gtgttgaaga aaactgcatt 360
 tatcatgagt ccaaattttt tggagtgaat ttccctgctg atggacctgt gatgaaaaag 420
 atgacagata actgggagcc atcctgcgag aagatcatac cagttacctaa gcaggggata 480
 ttgaaagggg atgtctccat gtacctcctt ctgaaggatg gtggcggtt acggtgccaa 540
 ttgcacacag ttacaaagc aaagtctgtg ccaagaaaga tgccggactg gcacttcatt 600
 cagcataagc tcacccgtga agaccgcagc gatgctaaga atcagaaatg gcatctgaca 660
 gaacatgcta ttgcatccgg atctgcattt ccc 693

<210> 4
 <211> 231
 <212> PRT
 <213> Zoanthus sp.

<400> 4
 Met Ala Gln Ser Lys His Gly Leu Thr Lys Glu Met Thr Met Lys Tyr
 1 5 10 15
 Arg Met Glu Gly Cys Val Asp Gly His Lys Phe Val Ile Thr Gly Glu
 20 25 30
 Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Ala Ile Asn Leu Cys Val
 35 40 45
 Val Glu Gly Gly Pro Leu Pro Phe Ala Glu Asp Ile Leu Ser Ala Ala
 50 55 60
 Phe Asn Tyr Gly Asn Arg Val Phe Thr Glu Tyr Pro Gln Asp Ile Ala
 65 70 75 80
 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Asp Arg Ser
 85 90 95
 Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Ala Asp Ile Thr

100	105	110
Val Ser Val Glu Glu Asn Cys Met Tyr His Glu Ser Lys Phe Tyr Gly		
115	120	125
Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Asp Asn		
130	135	140
Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Val Pro Lys Gln Gly Ile		
145	150	155
Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg		
165	170	175
Leu Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Arg		
180	185	190
Lys Met Pro Asp Trp His Phe Ile Gln His Lys Leu Thr Arg Glu Asp		
195	200	205
Arg Ser Asp Ala Lys Asn Gln Lys Trp His Leu Thr Glu His Ala Ile		
210	215	220
Ala Ser Gly Ser Ala Leu Pro		
225	230	

<210> 5
 <211> 865
 <212> DNA
 <213> Zoaanthus sp.

<400> 5
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 catggctcat tcaaaggcacg gtctaaaaga agaaatgaca atgaaatacc acatggaagg 120
 gtgcgtcaac ggacataaaat ttgtgatcac gggcgaaggc attggatatac cgttcaaagg 180
 gaaacagact attaatctgt gtgtgatcga agggggacca ttgccatttt ccgaagacat 240
 attgtcagct ggcttaagt acggagacag gattttact gaatatcctc aagacatagt 300
 agactatttc aagaactcgt gtcctgctgg atatacatgg ggcaggtctt ttctctttga 360
 ggtatggagca gtctgcataat gcaatgtaga tataacagtg agtgcataag aaaactgcac 420
 ttatcataag agcatattta atggaatgaa ttttcctgct gatggacctg tgatgaaaaa 480
 gatgacaact aactgggaag catcctgcga gaagatcatg ccagtaccta agcaggggat 540
 actgaaaggg gatgtctcca tgtacccct tctgaaggat ggtggcggtt accggtgcca 600
 gttcgacaca gtttacaaag caaagtctgt gccaagtaag atgcggaggt ggcacttcat 660
 ccagcataag ctccctccgtg aagaccgcag cgatgctaag aatcagaagt ggcagctgac 720
 agagcatgtc attgcattcc cttctgcctt ggcctgataa gaatgttagtt ccaacatttt 780
 aatgcatgtg cttgtcaatt attctgataa aaatgttagtt gagttgaaaa cagacaagta 840
 caaataaaagc acatgtaaat cgtct 865

<210> 6
 <211> 230
 <212> PRT
 <213> Zoaanthus sp.

<400> 6
 Met Ala His Ser Lys His Gly Leu Lys Glu Glu Met Thr Met Lys Tyr
 1 5 10 15
 His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu
 20 25 30
 Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val
 35 40 45
 Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly
 50 55 60
 Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val
 65 70 75 80
 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Ser Phe
 85 90 95
 Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr Val

100	105	110	
Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly Met			
115	120	125	
Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn Trp			
130	135	140	
Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile Leu			
145	150	155	160
Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr			
165	170	175	
Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys			
180	185	190	
Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg			
195	200	205	
Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala			
210	215	220	
Phe Pro Ser Ala Leu Ala			
225	230		

<210> 7
 <211> 678
 <212> DNA
 <213> Discosoma sp

<400> 7
 atgcgctcct ccaagaacgt catcaaggag ttcatgcgt tcaaggtgcg catggaggc 60
 accgtgaacg gccacgagtt cgagatcgag ggcgagggcg agggccgccc ctacgaggc 120
 cacaacaccg tgaagctgaa ggtgaccaag ggcggccccc tgcccttcgc ctggacatc 180
 ctgtcccccc agttccagta cggctccaag gtgtacgtg agcaccccg cgcacatcccc 240
 gactacaaga agctgtcctt ccccgagggc ttcaagtggg agcgcgtgat gaacttcgag 300
 gacggccggcg tggtgaccgt gacccaggac tccctccctgc aggacggctg cttcatctac 360
 aaggtgaagt tcatcggtgtaacttcccc tccgacggcc cctgtatgca gaagaagacc 420
 atgggctggg aggccctccac cgagcgcctg taccggccgc acggcgtgct gaagggccgag 480
 atccacaagg ccctgaagct gaaggacggc ggccactacc tggtgaggtt caagtccatc 540
 tacatggcca agaagcccgt gcagctgccc ggctactact acgtggactc caagctggac 600
 atcacctccc acaacgagga ctacaccatc gtggagcagt acgagcgcac cgagggccgc 660
 caccacctgt tcctgtaa 678

<210> 8
 <211> 225
 <212> PRT
 <213> Discosoma sp.

<400> 8
 Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val
 1 5 10 15
 Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
 20 25 30
 Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
 35 40 45
 Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
 50 55 60
 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
 65 70 75 80
 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
 85 90 95
 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
 100 105 110
 Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
 115 120 125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
 130 135 140
 Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
 145 150 155 160
 Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu
 165 170 175
 Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
 180 185 190
 Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
 195 200 205
 Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
 210 215 220
 Leu
 225

<210> 9
 <211> 696
 <212> DNA
 <213> Anemonia sulcata

<400> 9
 atggcttcct ttttaaagaa gactatgcc ttttaagacga ccattgaagg gacggtaat 60
 ggccactact tcaagtgtac aggaaaagga gagggcaacc catttgaggg tacgcaggaa 120
 atgaagatag aggtcatcga aggaggcata ttgcatttg cttccacat tttgtcaac 180
 agttgtatgt acggtatgaa ggccttcata aagtatgtgt caggaattcc tgactacttc 240
 aagcagtctt tccctgaagg ttttacttgg gaaagaacca caacctacga ggatggaggc 300
 tttcttacag ctcatcagga cacaagccta gatggagatt gcctcgat 360
 attcttgta ataattttcc tgctgatggc cccgtatgc agaacaaggc aggaagatgg 420
 gagccatcca ccgagatagt ttatgaagtt gacgggttcc tgcgtggaca gtcttgatg 480
 gcccctaagt gcccctgggg tcgtcatctg acttgcatac tccatactac ttacaggc 540
 aaaaaaccag ctgctgcctt gaagatgcca ggatttcatt ttgaagatca tcgcatacgag 600
 ataatggagg aagttgagaa aggcaagtgc tataaacagt acgaacgc acgtggcagg 660
 tactgtatgt ctgctccatc caagttgga cataac 696

<210> 10
 <211> 232
 <212> PRT
 <213> Anemonia sulcata

<400> 10
 Met Ala Ser Phe Leu Lys Lys Thr Met Pro Phe Lys Thr Thr Ile Glu
 1 5 10 15
 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Thr Gly Lys Gly Glu Gly
 20 25 30
 Asn Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly
 35 40 45
 Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr
 50 55 60
 Gly Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly
 100 105 110
 Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ala Thr
 130 135 140
 Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met

145	150	155	160												
Ala	Leu	Lys	Cys	Pro	Gly	Gly	Arg	His	Leu	Thr	Cys	His	Leu	His	Thr
				165		170						175			
Thr	Tyr	Arg	Ser	Lys	Lys	Pro	Ala	Ala	Ala	Leu	Lys	Met	Pro	Gly	Phe
				180		185						190			
His	Phe	Glu	Asp	His	Arg	Ile	Glu	Ile	Met	Glu	Glu	Val	Glu	Lys	Gly
				195		200					205				
Lys	Cys	Tyr	Lys	Gln	Tyr	Glu	Ala	Ala	Val	Gly	Arg	Tyr	Cys	Asp	Ala
				210		215					220				
Ala	Pro	Ser	Lys	Leu	Gly	His	Asn								
	225			230											

<210> 11
 <211> 678
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hybrid coding sequence

<400> 11
 atgagctgca gcaagaacgt gatcaaggag ttcatgcggc tcaaggtgcg gatggaggc 60
 accgtgaacg gccacgagtt cgagatcaag ggcgagggcg agggccggcc ctacgaggc 120
 cactgcagcg tgaagctcat ggtgaccaag ggcggccccc tcccttcgc cttcgacatc 180
 ctcagccccc agttccagta cggcagcaag gtgtacgtga agcacccccgc cgacatcccc 240
 gactacaaga agctcagctt ccccgaggc ttcagaatggg agcgggtgat gaacttcgag 300
 gacggcggcg tgggtgaccgt gagccaggac agcagcctca aggacggctg cttcatctac 360
 gaggtgaagt tcatacgccgt gaacttcccc agcgacggcc ccgtgatgca gcgccggacc 420
 cggggctggg aggccagcag cgagcggctc tacccccggg acggcgtgct caagggcgac 480
 atccacatgg ccctccggct cgagggcgcc ggccactacc tcgtggagtt caagagcata 540
 tacatggcca agaagcccggt gcagctcccc ggctactact acgtggacag caagctcgac 600
 atcaccagcc acaacgagga ctacaccatc gtggagcagt acgagcggac cgagggccgg 660
 caccacctct tcctctga 678

<210> 12
 <211> 225
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hybrid protein

<400> 12
 Met Ser Cys Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val
 1 5 10 15
 Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Lys Gly Glu
 20 25 30
 Gly Glu Gly Arg Pro Tyr Glu Gly His Cys Ser Val Lys Leu Met Val
 35 40 45
 Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser Pro Gln
 50 55 60
 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
 65 70 75 80
 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
 85 90 95
 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Ser Gln Asp Ser Ser
 100 105 110
 Leu Lys Asp Gly Cys Phe Ile Tyr Glu Val Lys Phe Ile Gly Val Asn
 115 120 125

Phe Pro Ser Asp Gly Pro Val Met Gln Arg Arg Thr Arg Gly Trp Glu
 130 135 140
 Ala Ser Ser Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Asp
 145 150 155 160
 Ile His Met Ala Leu Arg Leu Glu Gly Gly His Tyr Leu Val Glu
 165 170 175
 Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
 180 185 190
 Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
 195 200 205
 Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
 210 215 220
 Leu
 225

<210> 13
 <211> 675
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 13
 atggcctcct ccgagaacgt catcaccgag ttcatgcgt tcaaggtgcg catggaggc 60
 accgtgaacg gccacgagtt cgagatcgag ggcgagggcg agggccgccc ctacgaggc 120
 cacaacacccg tgaagctgaa ggtgaccaag ggccggccccc tgcccttcgc ctggacatc 180
 ctgtcccccc agttccagta cggctccaag gtgtacgtga agcacccccgc cgacatcccc 240
 gactacaaga agctgtcctt ccccgaggc ttcaagtggg agcgcgtgat gaacttcgag 300
 gacggccgcg tggcgaccgt gacccaggac tcctccctgc aggacggctg cttcatctac 360
 aaggtaagt tcatcgccgt gaacttcccc tccgacggcc ccgtgatgca gaagaagacc 420
 atgggctggg aggcctccac cgagcgcctg taccggcg agcgcgtgat gaagggcgag 480
 acccacaagg ccctgaagct gaaggacggc ggccactacc tggtgaggtt caagtccatc 540
 tacatggcca agaagcccggt gcagctgccc ggctactact acgtggacgc caagctggac 600
 atcacctccc acaacgagga ctacaccatc gtggagcagt acgagcgcac cgagggccgc 660
 caccacctgt tcctg 675

<210> 14
 <211> 678
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 14
 atggcctcct ccgagaacgt catcaccgag ttcatgcgt tcaaggtgcg catggaggc 60
 accgtgaacg gccacgagtt cgagatcgag ggcgagggcg agggccgccc ctacgaggc 120
 cacaacacccg tgaagttgaa ggtgaccaag ggccggccccc tgcccttcgc ctggacatc 180
 ctgtcccccc agttccagta cggctccaag gtgtacgtga agcacccccgc cgacatcccc 240
 gactacaaga agctgtcctt ccccgaggc ttcaagtggg agcgcgtgat gaacttcgag 300
 gacggccgcg tggcgaccgt gacccaggac tcctccctgc aggacggctg cttcatctac 360
 aaggtaagt tcatcgccgt gaacttcccc tccgacggcc ccgtgatgca gaagaagacc 420
 atgggctggg aggcctccac cgagcgcctg taccggcg agcgcgtgat gaagggcgag 480
 atccacaagg ccctgaagct gaaggacggc ggccactacc tggtgaggtt caagtccatc 540
 tacatggcca agaagcccggt gcagctgccc ggctactact acgtggacac caagctggac 600
 atcacctccc acaacgagga ctacaccatc gtggagcagt acgagcgcac cgagggccgc 660
 caccacctgt tcctgtaa 678

<210> 15
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> non-aggregating mutant

<400> 15
ggatccgctc agtcagagca cggtctaaca gaagaaatga caatgaaata ccgtatggaa 60
gggtgcgtcg atggacataa atttgtgatc acgggagagg gcattggata tccgttcaaa 120
gggaaacagg ctattaatct gtgtgtggtc gaaggtggac cattgccatt tgccgaagac 180
atattgtcag ctgcctttat gtacgaaac agggtttca ctgaatatcc tcaagacata 240
gttgactatt tcaagaactc gtgtcctgct ggatatacat gggacaggc ttttctctt 300
gaggatggag cagtttgcatt atgtaatgca gatataacag tgagtgtga agaaaactgc 360
atgtatcatg agtccaaatt ctatggatg aattttcctg ctgatggacc tttgtatgaaa 420
aagatgacag ataaactggg gccatcctgc gagaagatca taccagtacc taagcagggg 480
atattgaaag gggatgtctc catgtacctc cttctgaagg atggtggcg tttacgggtc 540
caattcgaca cagtttacaa agcaaagtct gtgccaagaa agatgcccga ctggcacttc 600
atccagcata agctcacccg tgaagaccgc agcgatgcta agaattcagaa atggcatctg 660
acagaacatg ctattgcattt cggatctgca ttgccctgaa agctt 705

<210> 16
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> non-aggregating mutant

<400> 16
Ala His Ser Glu His Gly Leu Thr Glu Glu Met Thr Met Lys Tyr His
1 5 10 15
Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly
20 25 30
Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val Ile
35 40 45
Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly Phe
50 55 60
Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val Asp
65 70 75 80
Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Arg Ser Phe
85 90 95
Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr Val
100 105 110
Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly Val
115 120 125
Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn Trp
130 135 140
Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile Leu
145 150 155 160
Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr
165 170 175
Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys
180 185 190
Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg
195 200 205
Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala
210 215 220
Phe Pro Ser Ala Leu Ala

<210> 17
 <211> 705
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> non-aggregating mutant

 <400> 17
 ggatccgccc acagcgagca cggcctgacc gaggagatga ccatgaagta ccacatggag 60
 ggctgcgtga acggccacaa gttcgtgatc accggcgagg gcatcggcta ccccttcaag 120
 ggcaagcaga ccatcaacct gtgcgtgatc gagggcgccc ccctgcccctt cagcgaggac 180
 atcctgagcg cccgcttcaa gtacggcgac cggatcttca ccgagtaacc ccaggacatc 240
 gtggactact tcaagaacag ctgccccgccc ggctacacct gggggcggag cttcctgttc 300
 gaggacggcg ccgtgtgcat ctgtaacgtg gacatcaccc tgagcgtgaa ggagaactgc 360
 atctaccaca agagcatctt caacggcggt aacttccccc ccgacggccc cgtgtatgaag 420
 aagatgacca ccaactggga ggccagctgc gagaagatca tgccctgtcc taagcagggc 480
 atcctgaagg ggcacgtgag catgtacctg ctgctgaagg acggcggccc gtaccgggtgc 540
 cagttcgaca ccgtgtacaa ggccaagagc gtgcccagca agatgcccga gtggcacttc 600
 atccagcaca agctgctgctg ggaggaccgg agcgacgcca agaaccagaa gtggcagctg 660
 accgagcacg ccatcgccctt ccccagcgcc ctggcctgaa agctt 705

 <210> 18
 <211> 230
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> non-aggregating mutant

 <400> 18
 Ala His Ser Glu His Gly Leu Thr Glu Glu Met Thr Met Lys Tyr His
 1 5 10 15
 Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly
 20 25 30
 Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val Ile
 35 40 45
 Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly Phe
 50 55 60
 Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val Asp
 65 70 75 80
 Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Arg Ser Phe
 85 90 95
 Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr Val
 100 105 110
 Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly Val
 115 120 125
 Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn Trp
 130 135 140
 Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile Leu
 145 150 155 160
 Lys Gly Asp Val Ser Met Tyr Leu Leu Lys Asp Gly Gly Arg Tyr
 165 170 175
 Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys
 180 185 190
 Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg
 195 200 205

Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala
210 215 220

Phe Pro Ser Ala Leu Ala
225 230

<210> 19
<211> 690
<212> DNA
<213> Artificial Sequence

<220>
<223> non-aggregating mutant

<400> 19
atggccctgt ccaacgagtt catcgcgac gacatgaaga tgacctacca catggacggc 60
tgcgtgaacg gccactactt caccgtgaag ggcgagggca gcggcaagcc ctacgaggc 120
acccagacct ccacacctaa ggtgaccatg gccaacggcg gccccctggc cttctccttc 180
gacatcctgt ccaccgtgtt catgtacggc aaccgctgt tcaccgccta ccccaccagc 240
atgcccact acttcaagca ggccttcccc gacggcatgt cctacgagag aaccttcacc 300
tacgaggacg gccgcgtggc caccgcgc gttggagatca gcctgaaggg caactgcttc 360
gagcacaagt ccacacctca cggcgtgaac ttccccggcc acggcccccgt gatggccaag 420
aagaccaccc gctgggaccc ctccctcgag aagatgacccg tgtgcgacgg catcttgaag 480
ggcgcacgtga ccgccttcct gatgctgcag ggcggcggca actacagatg ccagttccac 540
acctcctaca agaccaagaa gcccgtgacc atgcccccca accacgtggt ggagcaccgc 600
atcgccagaa ccgacacctga caagggcgcc aacagcgtgc agctgaccga gcacgcgtg 660
gcccacatca cctccgtggt gccccttcga 690

<210> 20
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> non-aggregating mutant

<400> 20
Met Ala Leu Ser Asn Glu Phe Ile Gly Asp Asp Met Lys Met Thr Tyr
1 5 10 15
His Met Asp Gly Cys Val Asn Gly His Tyr Phe Thr Val Lys Gly Glu
20 25 30
Gly Ser Gly Lys Pro Tyr Glu Gly Thr Gln Thr Ser Thr Phe Lys Val
35 40 45
Thr Met Ala Asn Gly Gly Pro Leu Ala Phe Ser Phe Asp Ile Leu Ser
50 55 60
Thr Val Phe Met Tyr Gly Asn Arg Cys Phe Thr Ala Tyr Pro Thr Ser
65 70 75 80
Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu
85 90 95
Arg Thr Phe Thr Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Glu
100 105 110
Ile Ser Leu Lys Gly Asn Cys Phe Glu His Lys Ser Thr Phe His Gly
115 120 125
Val Asn Phe Pro Ala Asp Gly Pro Val Met Ala Lys Lys Thr Thr Gly
130 135 140
Trp Asp Pro Ser Phe Glu Lys Met Thr Val Cys Asp Gly Ile Leu Lys
145 150 155 160
Gly Asp Val Thr Ala Phe Leu Met Leu Gln Gly Gly Gly Asn Tyr Arg
165 170 175
Cys Gln Phe His Thr Ser Tyr Lys Thr Lys Pro Val Thr Met Pro

180	185	190
Pro Asn His Val Val Glu His Arg Ile Ala Arg Thr Asp Leu Asp Lys		
195	200	205
Gly Gly Asn Ser Val Gln Leu Thr Glu His Ala Val Ala His Ile Thr		
210	215	220
Ser Val Val Pro Phe		
225		

<210> 21
<211> 707
<212> DNA
<213> Artificial Sequence

<220>
<223> non-aggregating mutant

<400> 21
ggatccgcct ccctgctgac cgagaccatg cccttcagga ccaccatcga gggcaccgtg 60
aacggccact acttcaagtg caccggcaag ggcgagggca accccctcga gggcaccagg 120
gagatgaaga tcgaggtgat cgagggcggc cccctgcct tcgccttcca catcctgtcc 180
acctcctgca tgtacggctc caaggccttc atcaagtacg tgcggcat cccgactac 240
ttcaagcagt ccctcccgaa gggcttcacc tgggagcgcg ccaccaccta cgaggacggc 300
ggcttcctga ccgcccacca ggacacactcc ctggacggcg actgccttgt gtacaagg 360
aagatcctgg gcaacaactt ccccgccgac ggccccgtga tgcagaacaa ggccggccgc 420
tgggagccct ccaccgagat cgtgtacgag gtggacggcg tgctgcgcgg ccagtccctg 480
atggccctgg atgtccccgg cggtcgccac ctgacctgcc acctgcacac cacctaccgc 540
tccaagaagc ccgcctccgc cctgaagatg cccggcttcc acttcgagga ccaccgcata 600
gagatcctgg aggaggtgga gaaggcgaag tgctacaagc agtacgaggc cgccgtggc 660
cgctactgca acgcccggcc ctccaagctg ggccacaact gaagctt 707

<210> 22
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> non-aggregating mutant

<400> 22
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Arg Thr Thr Ile Glu Gly
1 5 10 15
Thr Val Asn Gly His Tyr Phe Lys Cys Thr Gly Lys Gly Glu Gly Asn
20 25 30
Pro Leu Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35 40 45
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60
Ser Lys Ala Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80
Gln Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr Glu
85 90 95
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
100 105 110
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
115 120 125
Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ser Thr Glu
130 135 140
Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
145 150 155 160

Leu Glu Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr
 165 170 175
 Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His
 180 185 190
 Phe Glu Asp His Arg Ile Glu Ile Leu Glu Glu Val Glu Lys Gly Lys
 195 200 205
 Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala
 210 215 220
 Pro Ser Lys Leu Gly His Asn
 225 230

<210> 23
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 23
 gagggcaccg tgaacggcca ctacttcaag tgcaccggca agggcgaggg caaccccttc 60
 gagggcaccc aggagatgaa gatcgagggt atcgaggggcg gccccctgcc cttcgcccttc 120
 cacatccctgt ccacccctcg catgtacggc tccaaggccct tcatacaagta cgtgtccggc 180
 atccccgact acttcaagca gtcctccccc gagggcttca cctgggagcg caccaccacc 240
 tacgaggacg gcccgttcct gaccgcccac caggacaccc ctgggacccg cgactgcctg 300
 gtgtacaagg tgaagatcct gggcaacaac ttcccccggc acggcccccgt gatgcagaac 360
 aaggccggcc gctgggagcc ctccaccgag atcgtgtacg aggtggacgg cgtgctgcgc 420
 ggccagtcga gcatggccct ggagtcccc ggcggtcgcc acctgacctg ccacctgcac 480
 accacattacc gtcccaagaa gcccgcctcc gccctgaaga tgcccgctt ccacttcgag 540
 gaccacccgca tccagatcct ggaggaggtg gagaaggcca agtgtacaa gcagtacgag 600
 gccgcccgtgg gccgctactg cgacgcccgc ccctccaagc tggcccacaa ctga 654

<210> 24
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> non-aggregating mutant

<400> 24
 Met Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Arg Thr Thr Ile Glu
 1 5 10 15
 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Thr Gly Lys Glu Gly
 20 25 30
 Asn Pro Leu Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly
 35 40 45
 Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr
 50 55 60
 Gly Ser Lys Ala Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe
 65 70 75 80
 Lys Gln Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly
 100 105 110
 Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ser Thr
 130 135 140

Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Ser Met
145 150 155 160
Ala Leu Glu Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr
165 170 175
Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe
180 185 190
His Phe Glu Asp His Arg Ile Glu Ile Leu Glu Glu Val Glu Lys Gly
195 200 205
Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala
210 215 220
Ala Pro Ser Lys Leu Gly His Asn
225 230

<210> 25
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> non-aggregating mutant fragment

<400> 25
Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val
1 5 10 15
Arg Met Glu Gly Thr Val Asn Gly His Glu
20 25

<210> 26
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> non-aggregating mutant fragment

<400> 26
Met Ser Cys Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Gln Val
1 5 10 15
Arg Met Glu Gly Thr Val Asn Gly His Glu
20 25

<210> 27
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> non-aggregating mutant fragment

<400> 27
Met Ala Gln Ser Lys His Gly Leu Thr Lys Glu Met Thr Met Lys Tyr
1 5 10 15
Arg Met Glu Gly Cys Val Asp Gly His Lys
20 25

<210> 28

<211> 26
<212> PRT
<213> Artificial Sequence ¶

<220>
<223> non-aggregating mutant fragment

<400> 28
Met Ala His Ser Lys His Gly Leu Lys Glu Glu Met Thr Met Lys Tyr
1 5 10 15
His Met Glu Gly Cys Val Asn Gly His Lys
20 25

<210> 29
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> non-aggregating mutant fragment

<400> 29
Met Ala Leu Ser Asn Lys Phe Ile Gly Asp Asp Met Lys Met Thr Tyr
1 5 10 15
His Met Asp Gly Cys Val Asn Gly His Tyr
20 25

<210> 30
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> non-aggregating mutant fragment

<400> 30
Met Ala Ser Phe Leu Lys Lys Thr Met Pro Phe Lys Thr Thr Ile Glu
1 5 10 15
Gly Thr Val Asn Gly His Tyr
20

<210> 31
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> purification tag

<400> 31
Met Arg His His His His His Gly Ser
1 5 10